Amendment to the Claims:

Please amend the claims as follows.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claims 1 to 41 (canceled)

Claim 42 (currently amended): A method of generating a variant comprising:

obtaining a nucleic acid comprising a sequence selected from the group consisting of (a) a sequence comprising SEQ ID NO:7 or SEQ ID NO:5 (b) [[sequences substantially identical]] a sequence that hybridizes under stringent conditions to SEQ ID NO:7 or SEQ ID NO:5, wherein the stringent hybridization conditions comprise a wash step comprising 30 minutes at room temperature in a solution comprising 150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na_2EDTA containing 0.5% SDS, followed by a 30 minute wash in fresh solution at T_m-10°C, and the sequence encodes a polypeptide having catalase activity and is at least 35 residues in length, (c) a sequence [[fragments]] comprising at least 30 consecutive nucleotides of a sequence as set forth in SEQ ID NO:7 or at least 35 consecutive nucleotides of a sequence as set forth in SEQ ID NO:5, (d) a sequence having at least about [[50%]] 65% sequence identity to a sequence as set forth in SEQ ID NO:7 or SEQ ID NO:5, wherein the sequence encodes a polypeptide having catalase activity, and [[(d)]] (e) [[sequences]] a sequence complementary to (a), (b), (c) or (d); and

modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence.

Claim 43 (currently amended): The method of claim 42 or claim 93, wherein the modifications are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble

mutagenesis, site-specific mutagenesis, gene reassembly, [[gene site saturated mutagenesis (GSSM)]] Gene Site Saturation Mutagenesis™ (GSSM™), synthetic gene reassembly and any combination thereof.

Claim 44 (previously presented): The method of claim 42 or claim 93, wherein the modifications are introduced by error-prone PCR.

Claim 45 (previously presented): The method of claim 42 or claim 93, wherein the modifications are introduced by shuffling.

Claim 46 (previously presented): The method of claim 42 or claim 93, wherein the modifications are introduced by oligonucleotide-directed mutagenesis.

Claim 47 (previously presented): The method of claim 42 or claim 93, wherein the modifications are introduced by assembly PCR.

Claim 48 (previously presented): The method of claim 42 or claim 93, wherein the modifications are introduced by sexual PCR mutagenesis.

Claim 49 (previously presented): The method of claim 42 or claim 93, wherein the modifications are introduced by *in vivo* mutagenesis.

Claim 50 (previously presented): The method of claim 42 or claim 93, wherein the modifications are introduced by cassette mutagenesis.

Claim 51 (previously presented): The method of claim 42 or claim 93, wherein the modifications are introduced by recursive ensemble mutagenesis.

Claim 52 (previously presented): The method of claim 42 or claim 93, wherein the modifications are introduced by exponential ensemble mutagenesis.

Claim 53 (previously presented): The method of claim 42 or claim 93, wherein the modifications are introduced by site-specific mutagenesis.

Claim 54 (previously presented): The method of claim 42 or claim 93, wherein the modifications are introduced by gene reassembly.

Claims 55 to 92 (canceled)

Claim 93 (currently amended): A method of generating a variant comprising:

obtaining a nucleic acid comprising (a) a sequence ~~comprising SEQ ID NO:5, (b) a sequence having at least about 65% sequence identity to SEQ ID NO:5, (c) fragments~~ comprising at least about [[30]] 35 consecutive nucleotides of a sequence ~~as set forth in SEQ ID NO:5 or a sequence~~ having at least about 65% sequence identity to a sequence as set forth in SEQ ID NO:5 or at least about 30 consecutive nucleotides of a sequence having at least about 65% sequence identity to a sequence as set forth in SEQ ID NO:7, wherein the sequence encodes a polypeptide having catalase activity, or [[(d)]] (b) a sequence complementary to (a) [[, (b), (c) or (d)]]; and

modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence.

Claim 94 (previously presented): A method of generating a variant catalase comprising:

obtaining a nucleic acid comprising a sequence as set forth in SEQ ID NO:5 or SEQ ID NO:7; and

modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence, thereby generating a variant catalase.

Claim 95 to 97 (canceled)

Claim 98 (currently amended): The method of claim [[97]] 42, wherein the sequence has at least about 70% sequence identity to SEQ ID NO:7.

Claim 99 (previously presented): The method of claim 98, wherein the sequence has at least about 75% sequence identity to SEQ ID NO:7.

Claim 100 (previously presented): The method of claim 99, wherein the sequence has at least about 80% sequence identity to SEQ ID NO:7.

Claim 101 (previously presented): The method of claim 100, wherein the sequence has at least about 85% sequence identity to SEQ ID NO:7.

Claim 102 (previously presented): The method of claim 101, wherein the sequence has at least about 90% sequence identity to SEQ ID NO:7.

Claim 103 (previously presented): The method of claim 102, wherein the sequence has at least about 95% sequence identity to SEQ ID NO:7.

Claim 104 (previously presented): The method of claim 103, wherein the sequence has at least about 96% sequence identity to SEQ ID NO:7.

Claim 105 (currently amended): The method of claim 104, wherein the sequence has at least about 97% sequence identity to SEQ ID NO:7.

Claim 106 (previously presented): The method of claim 105, wherein the sequence has at least about 98% sequence identity to SEQ ID NO:7.

Claim 107 (previously presented): The method of claim 106, wherein the sequence has at least about 99% sequence identity to SEQ ID NO:7.

Claim 108 (currently amended): The method of claim [[97]] 42, wherein the sequence has at least about 70% sequence identity to SEQ ID NO:5.

Claim 109 (previously presented): The method of claim 108, wherein the sequence has at least about 75% sequence identity to SEQ ID NO:5.

Claim 110 (previously presented): The method of claim 109, wherein the sequence has at least about 80% sequence identity to SEQ ID NO:5.

Claim 111 (previously presented): The method of claim 110, wherein the sequence has at least about 85% sequence identity to SEQ ID NO:5.

Claim 112 (previously presented): The method of claim 111, wherein the sequence has at least about 90% sequence identity to SEQ ID NO:5.

Claim 113 (previously presented): The method of claim 112, wherein the sequence has at least about 95% sequence identity to SEQ ID NO:5.

Claim 114 (previously presented): The method of claim 113, wherein the sequence has at least about 96% sequence identity to SEQ ID NO:5.

Claim 115 (previously presented): The method of claim 114, wherein the sequence has at least about 97% sequence identity to SEQ ID NO:5.

Claim 116 (previously presented): The method of claim 115, wherein the sequence has at least about 98% sequence identity to SEQ ID NO:5.

Claim 117 (previously presented): The method of claim 116, wherein the sequence has at least about 99% sequence identity to SEQ ID NO:5.

Claim 118 (new): The method of claim 42 or claim 93, wherein the modifications are introduced by Gene Site Saturation Mutagenesis™ (GSSM™).

Claim 119 (new): The method of claim 42 or claim 93, wherein the modifications are introduced by synthetic gene reassembly.